



## SEQUENCE LISTING

<110> HUGANIR, RICHARD L.  
KIM, GJEEHAE

<120> SIGNAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF

<130> 48235/1699

<140> 09/294,298

<141> 1999-04-19

<150> 60/082,690

<151> 1998-04-22

<150> 60/082,717

<151> 1998-04-23

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 4272

<212> DNA

<213> Unknown Organism

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<223> Description of Unknown Organism: mammalian  
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<221> CDS

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Ser	Ala	Glu	Met	Gln	Gly	Tyr	Met	Met	Arg	Asp	Leu	Asn	Ser	Ser	Ile	
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Asp	Thr	Val	Phe	Trp	Gly	Glu	His	Phe	Glu	Phe	Asn	Asn	Leu	Pro	Ala	290	295	300
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Phe	Leu	Ser	Asp	Met	Ala	Met	Ser	Glu	Val	Asp	Arg	Phe	Met	Glu	Arg	450	455	460
Glu	His	Leu	Ile	Phe	Arg	Glu	Asn	Thr	Leu	Ala	Thr	Lys	Ala	Ile	Glu	465	470	475
Glu	Tyr	Met	Arg	Leu	Ile	Gly	Gln	Lys	Tyr	Leu	Lys	Asp	Ala	Ile	Gly	485	490	495
Glu	Phe	Ile	Arg	Ala	Leu	Tyr	Glu	Ser	Glu	Glu	Asn	Cys	Glu	Val	Asp	500	505	510
Pro	Ile	Lys	Cys	Thr	Ala	Ser	Ser	Leu	Ala	Glu	His	Gln	Ala	Asn	Leu	515	520	525
Arg	Met	Cys	Cys	Glu	Leu	Ala	Leu	Cys	Lys	Val	Val	Asn	Ser	His	Cys	530	535	540
Val	Phe	Pro	Arg	Glu	Leu	Lys	Glu	Val	Phe	Ala	Ser	Trp	Arg	Leu	Arg	545	550	555
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Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala  
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 Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu  
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 Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe  
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 Gly Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg  
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 Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu  
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 Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln  
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 Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu  
 835 840 845  
 Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala  
 850 855 860

Ala	Leu	Gly	Leu	Arg	Pro	Ala	Pro	Ala	Gly	Arg	Leu	Ser	Gln	Gly	Ser	865	870	875	880
Gly	Ser	Ser	Ile	Thr	Ala	Ala	Gly	Met	Arg	Leu	Ser	Gln	Met	Gly	Val		885	890	895
Thr	Thr	Asp	Gly	Val	Pro	Ala	Gln	Gln	Leu	Arg	Ile	Pro	Leu	Ser	Phe		900	905	910
Gln	Asn	Pro	Leu	Phe	His	Met	Ala	Ala	Asp	Gly	Pro	Gly	Pro	Pro	Ala		915	920	925
Gly	His	Gly	Gly	Ser	Ser	Gly	His	Gly	Pro	Pro	Ser	Ser	His	His	His	930	935	940	
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Phe	Ala	Pro	Phe	His	Gly	Tyr	Ser	Lys	Ser	Glu	Asp	Leu	Ser	Thr	Gly		965	970	975
Val	Pro	Lys	Pro	Pro	Ala	Ala	Ser	Ile	Leu	His	Ser	His	Ser	Tyr	Ser		980	985	990
Asp	Glu	Phe	Gly	Pro	Ser	Gly	Thr	Asp	Phe	Thr	Arg	Arg	Gln	Leu	Ser		995	1000	1005
Leu	Gln	Asp	Asn	Leu	Gln	His	Met	Leu	Ser	Pro	Pro	Gln	Ile	Thr	Ile	1010	1015	1020	
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Lys	Ser	Gln	Gln	Leu	Thr	Val	Ser	Ala	Ala	Gln	Lys	Pro	Arg	Pro	Ser		1060	1065	1070
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Pro	Arg	Gln	Gln	Ser	Leu	Ser	Lys	Glu	Gly	Ser	Ile	Gly	Gly	Ser	Gly	1090	1095	1100	
Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Leu	Lys	Pro	Ser	Ile	Thr	Lys	1105	1110	1115	1120
Gln	His	Ser	Gln	Thr	Pro	Ser	Thr	Leu	Asn	Pro	Thr	Met	Pro	Ala	Ser		1125	1130	1135
Glu	Arg	Thr	Val	Ala	Trp	Val	Ser	Asn	Met	Pro	His	Leu	Ser	Ala	Asp		1140	1145	1150
Ile	Glu	Ser	Ala	His	Ile	Glu	Arg	Glu	Glu	Tyr	Lys	Leu	Lys	Glu	Tyr	1155	1160	1165	

Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu  
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 Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys  
 1185 1190 1195 1200  
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 Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg  
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<212> DNA

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<220>

<223> Description of Unknown Organism: mammalian  
SYNGAP-B

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tgc ccc ctc ctt ccc acc gcc agc ctc tcc gcc gcc gct gct ctt cct	96
Cys Pro Leu Leu Pro Thr Ala Ser Leu Ser Ala Ala Ala Ala Leu Pro	
20 25 30	
gct gct ttc cgg ggg aat acc act tgg gtc gct cga gga gga aga gtg	144
Ala Ala Phe Arg Gly Asn Thr Thr Trp Val Ala Arg Gly Gly Arg Val	
35 40 45	
tcc ccg ggg ggg aaa cag tac agc atg gaa gcc gcc ccc gct gcg ccc	192
Ser Pro Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro	
50 55 60	
ttc cgg ccc tcg caa ggc ttc ctg agc cgg agg cta aaa agc tcc atc	240
Phe Arg Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile	
65 70 75	
aaa cgt aca aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga	288
Lys Arg Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg	
80 85 90 95	
cag atc ctg cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg	336
Gln Ile Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu	
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atg cag agc ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc	384
Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro	
115 120 125	
agc agt gct gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att	432
Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile	
130 135 140	
atc aag cca gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag	480
Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu	
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gta aca aca tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc	528
Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala	
160 165 170 175	
gaa agg gac aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac	576
Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn	
180 185 190	
aag gac aac agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata	624
Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile	
195 200 205	

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Glu Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys	
210 215 220	
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Leu Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala	
225 230 235	
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Ser Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu	
240 245 250 255	
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Pro Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys	
260 265 270	
aag cgg aag aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca	864
Lys Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro	
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Val Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val	
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Thr Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly	
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Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys	
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Met Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg	
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atg ctg tgt gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag	1152
Met Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu	
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Glu Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala	
385 390 395	
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Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met	
400 405 410 415	
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gta gac ccc atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala 465 470 475	1440
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ccg	agc	cgc	cag	agc	gag	cgc	gct	cgg	tct	cag	ccc	atg	gtg	ctg	cgc	2064
Pro	Ser	Arg	Gln 675	Ser	Glu	Arg	Ala	Arg 680	Ser	Gln	Pro	Met	Val 685	Leu	Arg	
ggg	ccg	tca	gcc	gag	atg	cag	ggc	tac	atg	atg	cgg	gac	ctc	aac	agc	2112
Gly	Pro	Ser 690	Ala	Glu	Met	Gln	Gly 695	Tyr	Met	Met	Arg	Asp 700	Leu	Asn	Ser	
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Ser	Ile 705	Asp	Leu	Gln	Ser	Phe 710	Met	Ala	Arg	Gly	Leu 715	Asn	Ser	Ser	Met	
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Asp 720	Met	Ala	Arg	Leu 725	Pro	Ser	Pro	Thr	Lys	Glu 730	Lys	Pro	Pro	Pro	Pro 735	
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Thr	Ala	Ala	Leu 820	Gly	Leu	Arg	Pro	Ala	Pro 825	Ala	Gly	Arg	Leu 830	Ser	Gln	
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 Pro His Pro  
           1375

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<220>  
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           SYNGAP-B

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 Pro Leu Leu Pro Thr Ala Ser Leu Ser Ala Ala Ala Ala Leu Pro Ala  
                   20                  25                  30  
 Ala Phe Arg Gly Asn Thr Thr Trp Val Ala Arg Gly Gly Arg Val Ser  
                   35                  40                  45  
 Pro Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro Phe  
           50                  55                  60  
 Arg Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys  
   65                  70                  75                  80  
 Arg Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln  
                   85                  90                  95  
 Ile Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met  
                   100                  105                  110  
 Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser  
           115                  120                  125  
 Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile  
           130                  135                  140  
 Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val  
   145                  150                  155                  160

Thr	Thr	Ser	Ser	Gly	Thr	Lys	Cys	Phe	Ala	Cys	Arg	Ser	Ala	Ala	Glu	
				165					170					175		
Arg	Asp	Lys	Trp	Ile	Glu	Asn	Leu	Gln	Arg	Ala	Val	Lys	Pro	Asn	Lys	
			180					185					190			
Asp	Asn	Ser	Arg	Arg	Val	Asp	Asn	Val	Leu	Lys	Leu	Trp	Ile	Ile	Glu	
		195					200					205				
Ala	Arg	Glu	Leu	Pro	Pro	Lys	Lys	Arg	Tyr	Tyr	Cys	Glu	Leu	Cys	Leu	
	210					215					220					
Asp	Asp	Met	Leu	Tyr	Ala	Arg	Thr	Thr	Ser	Lys	Pro	Arg	Ser	Ala	Ser	
225					230					235					240	
Gly	Asp	Thr	Val	Phe	Trp	Gly	Glu	His	Phe	Glu	Phe	Asn	Asn	Leu	Pro	
				245					250					255		
Ala	Val	Arg	Ala	Leu	Arg	Leu	His	Leu	Tyr	Arg	Asp	Ser	Asp	Lys	Lys	
			260					265					270			
Arg	Lys	Lys	Asp	Lys	Ala	Gly	Tyr	Val	Gly	Leu	Val	Thr	Val	Pro	Val	
		275					280					285				
Ala	Thr	Leu	Ala	Gly	Arg	His	Phe	Thr	Glu	Gln	Trp	Tyr	Pro	Val	Thr	
	290					295					300					
Leu	Pro	Thr	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Met	Gly	Ser	Gly	Gly	Gly	
305					310					315					320	
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Lys	Gly	Lys	Gly	Gly	Cys	Pro	
				325					330					335		
Ala	Val	Arg	Leu	Lys	Ala	Arg	Tyr	Gln	Thr	Met	Ser	Ile	Leu	Pro	Met	
			340					345					350			
Glu	Leu	Tyr	Lys	Glu	Phe	Ala	Glu	Tyr	Val	Thr	Asn	His	Tyr	Arg	Met	
		355					360					365				
Leu	Cys	Ala	Val	Leu	Glu	Pro	Ala	Leu	Asn	Val	Lys	Gly	Lys	Glu	Glu	
	370					375					380					
Val	Ala	Ser	Ala	Leu	Val	His	Ile	Leu	Gln	Ser	Thr	Gly	Lys	Ala	Lys	
385					390					395					400	
Asp	Phe	Leu	Ser	Asp	Met	Ala	Met	Ser	Glu	Val	Asp	Arg	Phe	Met	Glu	
				405					410					415		
Arg	Glu	His	Leu	Ile	Phe	Arg	Glu	Asn	Thr	Leu	Ala	Thr	Lys	Ala	Ile	
			420					425					430			
Glu	Glu	Tyr	Met	Arg	Leu	Ile	Gly	Gln	Lys	Tyr	Leu	Lys	Asp	Ala	Ile	
		435					440					445				
Gly	Glu	Phe	Ile	Arg	Ala	Leu	Tyr	Glu	Ser	Glu	Glu	Asn	Cys	Glu	Val	
	450					455						460				

Asp	Pro	Ile	Lys	Cys	Thr	Ala	Ser	Ser	Leu	Ala	Glu	His	Gln	Ala	Asn	465	470	475	480
Leu	Arg	Met	Cys	Cys	Glu	Leu	Ala	Leu	Cys	Lys	Val	Val	Asn	Ser	His		485	490	495
Cys	Val	Phe	Pro	Arg	Glu	Leu	Lys	Glu	Val	Phe	Ala	Ser	Trp	Arg	Leu		500	505	510
Arg	Cys	Ala	Glu	Arg	Gly	Arg	Glu	Asp	Ile	Ala	Asp	Arg	Leu	Ile	Ser		515	520	525
Ala	Ser	Leu	Phe	Leu	Arg	Phe	Leu	Cys	Pro	Ala	Ile	Met	Ser	Pro	Ser		530	535	540
Leu	Phe	Gly	Leu	Met	Gln	Glu	Tyr	Pro	Asp	Glu	Gln	Thr	Ser	Arg	Thr	545	550	555	560
Leu	Thr	Leu	Ile	Ala	Lys	Val	Ile	Gln	Asn	Leu	Ala	Asn	Phe	Ser	Lys		565	570	575
Phe	Thr	Ser	Lys	Glu	Asp	Phe	Leu	Gly	Phe	Met	Asn	Glu	Phe	Leu	Glu		580	585	590
Leu	Glu	Trp	Gly	Ser	Met	Gln	Gln	Phe	Leu	Tyr	Glu	Ile	Ser	Asn	Leu		595	600	605
Asp	Thr	Leu	Thr	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Tyr	Ile	Asp	Leu	Gly	610	615	620	
Arg	Glu	Leu	Ser	Thr	Leu	His	Ala	Leu	Leu	Trp	Glu	Val	Leu	Pro	Gln	625	630	635	640
Leu	Ser	Lys	Glu	Ala	Leu	Leu	Lys	Leu	Gly	Pro	Leu	Pro	Arg	Leu	Leu		645	650	655
Ser	Asp	Ile	Ser	Thr	Ala	Leu	Arg	Asn	Pro	Asn	Ile	Gln	Arg	Gln	Pro		660	665	670
Ser	Arg	Gln	Ser	Glu	Arg	Ala	Arg	Ser	Gln	Pro	Met	Val	Leu	Arg	Gly		675	680	685
Pro	Ser	Ala	Glu	Met	Gln	Gly	Tyr	Met	Met	Arg	Asp	Leu	Asn	Ser	Ser	690	695	700	
Ile	Asp	Leu	Gln	Ser	Phe	Met	Ala	Arg	Gly	Leu	Asn	Ser	Ser	Met	Asp	705	710	715	720
Met	Ala	Arg	Leu	Pro	Ser	Pro	Thr	Lys	Glu	Lys	Pro	Pro	Pro	Pro	Pro		725	730	735
Pro	Gly	Gly	Gly	Lys	Asp	Leu	Phe	Tyr	Val	Ser	Arg	Pro	Pro	Leu	Ala		740	745	750
Arg	Ser	Ser	Pro	Ala	Tyr	Cys	Thr	Ser	Ser	Ser	Asp	Ile	Thr	Glu	Pro	755	760	765	

Glu	Gln	Lys	Met	Leu	Ser	Val	Asn	Lys	Ser	Val	Ser	Met	Leu	Asp	Leu	770	775	780	
Gln	Gly	Asp	Gly	Pro	Gly	Gly	Arg	Leu	Asn	Ser	Ser	Ser	Val	Ser	Asn	785	790	795	800
Leu	Ala	Ala	Val	Gly	Asp	Leu	Leu	His	Ser	Ser	Gln	Ala	Ser	Leu	Thr	805	810	815	
Ala	Ala	Leu	Gly	Leu	Arg	Pro	Ala	Pro	Ala	Gly	Arg	Leu	Ser	Gln	Gly	820	825	830	
Ser	Gly	Ser	Ser	Ile	Thr	Ala	Ala	Gly	Met	Arg	Leu	Ser	Gln	Met	Gly	835	840	845	
Val	Thr	Thr	Asp	Gly	Val	Pro	Ala	Gln	Gln	Leu	Arg	Ile	Pro	Leu	Ser	850	855	860	
Phe	Gln	Asn	Pro	Leu	Phe	His	Met	Ala	Ala	Asp	Gly	Pro	Gly	Pro	Pro	865	870	875	880
Ala	Gly	His	Gly	Gly	Ser	Ser	Gly	His	Gly	Pro	Pro	Ser	Ser	His	His	885	890	895	
His	His	His	His	His	His	His	His	Arg	Gly	Gly	Glu	Pro	Pro	Gly	Asp	900	905	910	
Thr	Phe	Ala	Pro	Phe	His	Gly	Tyr	Ser	Lys	Ser	Glu	Asp	Leu	Ser	Thr	915	920	925	
Gly	Val	Pro	Lys	Pro	Pro	Ala	Ala	Ser	Ile	Leu	His	Ser	His	Ser	Tyr	930	935	940	
Ser	Asp	Glu	Phe	Gly	Pro	Ser	Gly	Thr	Asp	Phe	Thr	Arg	Arg	Gln	Leu	945	950	955	960
Ser	Leu	Gln	Asp	Asn	Leu	Gln	His	Met	Leu	Ser	Pro	Pro	Gln	Ile	Thr	965	970	975	
Ile	Gly	Pro	Gln	Arg	Pro	Ala	Pro	Ser	Gly	Pro	Gly	Gly	Gly	Ser	Gly	980	985	990	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gln	Pro	Pro	Pro	Leu	Gln	Arg	995	1000	1005	
Gly	Lys	Ser	Gln	Gln	Leu	Thr	Val	Ser	Ala	Ala	Gln	Lys	Pro	Arg	Pro	1010	1015	1020	
Ser	Ser	Gly	Asn	Leu	Leu	Gln	Ser	Pro	Glu	Pro	Ser	Tyr	Gly	Pro	Ala	1025	1030	1035	1040
Arg	Pro	Arg	Gln	Gln	Ser	Leu	Ser	Lys	Glu	Gly	Ser	Ile	Gly	Gly	Ser	1045	1050	1055	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Leu	Lys	Pro	Ser	Ile	Thr	1060	1065	1070	



Lys Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala  
 1075 1080 1085  
 Ser Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala  
 1090 1095 1100  
 Asp Ile Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu  
 1105 1110 1115 1120  
 Tyr Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr  
 1125 1130 1135  
 Glu Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg  
 1140 1145 1150  
 Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr  
 1155 1160 1165  
 Ser Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys  
 1170 1175 1180  
 Arg Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile  
 1185 1190 1195 1200  
 Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro  
 1205 1210 1215  
 Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala  
 1220 1225 1230  
 Gln Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp  
 1235 1240 1245  
 Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro  
 1250 1255 1260  
 Gly Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr  
 1265 1270 1275 1280  
 Ser Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly  
 1285 1290 1295  
 Pro Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr  
 1300 1305 1310  
 Ser Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser  
 1315 1320 1325  
 Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His  
 1330 1335 1340  
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 SYNGAP-C

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cag caa ggc ttc ctg agc cgg agg cta aaa agc tcc atc aaa cgt aca 96  
     Gln Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr 30  
                     20                    25                    30

aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga cag atc ctg 144  
     Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu 45  
                     35                    40                    45

cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg atg cag agc 192  
     Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser 60  
                     50                    55                    60

ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc agc agt gct 240  
     Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala 75  
                     65                    70                    75

gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att atc aag cca 288  
     Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro 95  
         80                    85                    90                    95

gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag gta aca aca 336  
     Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr 110  
                     100                    105                    110

tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc gaa agg gac 384  
     Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp 125  
                     115                    120                    125

aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac aag gac aac 432  
     Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn 140  
                     130                    135                    140

agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata gaa gct cga 480  
     Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg 155  
                     145                    150                    155

gag ctg ccc ccc aag aag cga tat tac tgc gag tta tgc ctg gac gac 528  
     Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp 175  
         160                    165                    170                    175

atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc tca gga gac	576
Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp	
180 185 190	
act gtc ttt tgg ggc gag cac ttc gag ttt aac aac ctg cct gct gtc	624
Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val	
195 200 205	
cgg gcg ctg cgg ctg cat ctg tac cgt gac tcg gac aaa aag cgg aag	672
Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys	
210 215 220	
aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca gtg gcc acc	720
Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr	
225 230 235	
ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg acc ctg cca	768
Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro	
240 245 250 255	
aca gga agt ggg ggc tct ggg ggt atg ggc tcg ggg gga gga ggg ggg	816
Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly Gly Gly	
260 265 270	
tca ggg ggc ggc tca ggg ggc aaa ggg aaa gga ggc tgt cct gct gtg	864
Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro Ala Val	
275 280 285	
cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc atg gag cta	912
Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu Leu	
290 295 300	
tat aag gag ttt gca gaa tat gtg acc aac cac tac cgc atg ctg tgt	960
Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys	
305 310 315	
gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag gag gtc gct	1008
Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala	
320 325 330 335	
agt gca ctg gtt cac atc ctg caa agc aca ggc aag gcc aag gac ttc	1056
Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys Asp Phe	
340 345 350	
ctt tca gac atg gcc atg tca gag gta gac cgg ttc atg gag cgg gaa	1104
Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg Glu	
355 360 365	
cac ctc ata ttc cgc gag aac acg ctc gcc act aaa gcc ata gaa gag	1152
His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu Glu	
370 375 380	
tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc att ggg gag	1200
Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu	
385 390 395	

ttc atc cgg gct ctg tat gaa tct gag gag aac tgt gaa gta gac ccc	1248
Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro	
400 405 410 415	
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Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu Arg	
420 425 430	
atg tgc tgt gag ttg gcc ctg tgc aag gtg gtc aac tcc cat tgc gtg	1344
Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys Val	
435 440 445	
ttc ccg agg gag ctg aag gag gtg ttt gca tca tgg cgg ctg cgc tgt	1392
Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg Cys	
450 455 460	
gca gag cgg ggc cgg gag gac att gct gac agg ctg atc agc gcc tcg	1440
Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala Ser	
465 470 475	
ctc ttc ctg cgc ttc ctc tgc ccg gcc atc atg tcg ccc agt ctg ttt	1488
Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe	
480 485 490 495	
gga ctg atg cag gag tac cca gat gag cag acc tca cga acc ctc acc	1536
Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu Thr	
500 505 510	
ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc aag ttt acc	1584
Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe Thr	
515 520 525	
tca aag gag gac ttc ctg ggc ttc atg aac gag ttt ctg gag ctg gaa	1632
Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu Glu	
530 535 540	
tgg ggt tct atg cag caa ttc ttg tat gag ata tcc aac ctg gac aca	1680
Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp Thr	
545 550 555	
ctg acc aac agc agc agt ttt gag ggc tac ata gac ttg ggc cgc gag	1728
Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg Glu	
560 565 570 575	
ctc tcc aca ctt cac gcc ctg ctc tgg gag gtg ctg ccc cag ctc agc	1776
Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu Ser	
580 585 590	
aag gaa gcc ctc ctg aag ctg ggc ccg ctg ccc cgg ctc ctc agc gac	1824
Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser Asp	
595 600 605	
atc agc aca gcc ctg agg aac cct aac atc caa agg cag ccg agc cgc	1872
Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser Arg	
610 615 620	

cag agc gag cgc gct cgg tct cag ccc atg gtg ctg cgc ggg ccg tca Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly Pro Ser 625 630 635	1920
gcc gaa atg cag ggc tac atg atg cgg gac ctc aac agc tcc atc gac Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile Asp 640 645 650 655	1968
ctt cag tcc ttc atg gct cga ggc ctc aac agc tct atg gac atg gct Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met Ala 660 665 670	2016
cgc ctc ccc tcc cca acc aag gag aaa ccc ccg ccg ccc cct ccc ggt Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro Gly 675 680 685	2064
ggg ggt aaa gac ctg ttc tat gtg agc cgg cca cca ctg gcc cgg tcc Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg Ser 690 695 700	2112
tcc cca gca tac tgc acg agc agc tcg gac atc aca gag ccg gag cag Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu Gln 705 710 715	2160
aag atg ctg agt gtc aac aag agt gtg tcc atg ctg gac ctg cag ggc Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln Gly 720 725 730 735	2208
gac ggg cct ggg ggc cgc ctt aac agc agt agt gtt tcc aac ctg gca Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu Ala 740 745 750	2256
gct gtt ggg gac ctg ttg cac tca agc cag gct tca ctg aca gca gcc Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala Ala 755 760 765	2304
ttg ggg ttg cgg cct gca cct gcc ggg cgc ctc tcc caa ggg agt ggc Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser Gly 770 775 780	2352
tct tcc atc aca gca gcc ggc atg cgc ctc agc cag atg ggt gtc act Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val Thr 785 790 795	2400
acg gat ggt gtc ccc gcc cag caa ctg cgc atc cct ctt tcc ttc cag Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe Gln 800 805 810 815	2448
aac cct ctc ttc cat atg gct gcc gat gga cca ggg ccc cca gca ggc Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly 820 825 830	2496
cat gga ggg agc agt ggc cat ggt cca cct tcc tcc cat cac cac cac His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His His 835 840 845	2544

cac cac cat cac cat cac cga ggg gga gaa ccc cca ggg gac act ttt His His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr Phe 850 855 860	2592
gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct aca ggg gtc Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val 865 870 875	2640
cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc tac agt gat Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp 880 885 890 895	2688
gag ttt gga ccc tct ggt act gat ttt acc cgt cgg cag ctc tca ctt Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu 900 905 910	2736
cag gac aac cta cag cac atg ctc tcc ccg ccc cag atc acc atc ggt Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly 915 920 925	2784
ccc cag agg cca gct ccc tca ggg cca gga ggg ggc agt ggt ggg ggc Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly Gly Gly 930 935 940	2832
agt ggt ggg ggc ggt ggg ggc cag cca cct ccc ttg cag agg ggc aaa Ser Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys 945 950 955	2880
tct cag cag ttg aca gtg agt gct gcc cag aaa ccc cgg ccg tcc agc Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser 960 965 970 975	2928
ggg aac cta ttg cag tcc ccg gaa cca agt tat ggt cct gcc cgt cca Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro 980 985 990	2976
cgg caa cag agc ctc agc aaa gag ggc agc att ggg ggc agc ggg ggc Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly 995 1000 1005	3024
agc ggt ggc gga ggg ggt ggg ggg ctc aag ccc tcc atc acc aag cag Ser Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln 1010 1015 1020	3072
cat tcc cag act cca tcc acg ctg aac ccc acg atg ccg gcc tcg gag His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu 1025 1030 1035	3120
cgg act gta gcc tgg gtg tcc aat atg cct cac ctg tcc gct gac atc Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile 1040 1045 1050 1055	3168
gag agt gca cac att gag cgg gaa gag tac aag ctg aag gag tac tcg Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser 1060 1065 1070	3216

aag tcc atg gac gag agc cga ctg gac agg gtg aag gag tac gag gag Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu 1075 1080 1085	3264
gag atc cac tca ctg aag gaa agg cta cac atg tcc aac cgg aag ctg Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu 1090 1095 1100	3312
gaa gag tac gag cgg agg ctg ctg tcc cag gaa gag cag acc agc aag Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys 1105 1110 1115	3360
atc ctg atg cag tac caa gcc cgc ctg gag cag agc gag aag cgc ttg Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg Leu 1120 1125 1130 1135	3408
agg cag cag cag gtg gag aag gac tcc cag atc aag agc atc att ggc Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile Gly 1140 1145 1150	3456
agg ctg atg ctg gtg gag gag gag ctg cgc cgg gac cac ccc gcc atg Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro Ala Met 1155 1160 1165	3504
gct gag ccg ctg cct gaa ccc aag aag agg ctg ctc gac gct cag aga Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg 1170 1175 1180	3552
ggc agc ttc ccc cct tgg gtc caa caa acc cgc gtg tga cgc tgg ccc Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro 1185 1190 1195	3600
cac ctt gga acg gcc tgg ccc ccc cag ccc cac ccc ccc cac ccc ggc His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly 1200 1205 1210	3648
tgc aga tca cag aga acg gcg agt tcc gga aca ccg cag acc act agc Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser 1215 1220 1225 1230	3696
cca ccc agc atc aca gac ctc ctt ccc tgt gca ccc tac ccc ggc cca Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro 1235 1240 1245	3744
ccc agc gtc aca gac ctc ctt ccc agt gca ccc gac cct gga aca tca Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser 1250 1255 1260	3792
cca acc acc agg act gga cgt cac caa ggg aca gcg gga ttg tct ccc Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro 1265 1270 1275	3840
tta acg cct cct tgg ggc acc cat ctg tca acc cca ctg ctc cat tcc Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser 1280 1285 1290	3888



agg agg gag agt ggg acc ctc agc tgc cct ctc acc cca gga cac cac 3936  
 Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His  
 1295 1300 1305 1310

cta ccc cac aca gac ccc ttc act ctg ggg tgc tat ccc cat cct 3981  
 Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro  
 1315 1320 1325

<210> 6

<211> 1325

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian  
 SYNGAP-C

<400> 6

Gly Glu Thr Glu Leu Pro Gln Ala Pro His Phe Pro Phe Ala Pro Gln  
 1 5 10 15

Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr Lys  
 20 25 30

Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu Pro  
 35 40 45

Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser Phe  
 50 55 60

Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala Ala  
 65 70 75 80

Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro Val  
 85 90 95

His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr Ser  
 100 105 110

Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp Lys  
 115 120 125

Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn Ser  
 130 135 140

Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu  
 145 150 155 160

Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met  
 165 170 175

Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr  
 180 185 190

Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg  
 195 200 205

Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys  
 210 215 220  
 Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu  
 225 230 235 240  
 Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr  
 245 250 255  
 Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly Gly Gly Ser  
 260 265 270  
 Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro Ala Val Arg  
 275 280 285  
 Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu Leu Tyr  
 290 295 300  
 Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys Ala  
 305 310 315 320  
 Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala Ser  
 325 330 335  
 Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys Asp Phe Leu  
 340 345 350  
 Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg Glu His  
 355 360 365  
 Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu Glu Tyr  
 370 375 380  
 Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu Phe  
 385 390 395 400  
 Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro Ile  
 405 410 415  
 Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu Arg Met  
 420 425 430  
 Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys Val Phe  
 435 440 445  
 Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg Cys Ala  
 450 455 460  
 Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala Ser Leu  
 465 470 475 480  
 Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe Gly  
 485 490 495  
 Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu Thr Leu  
 500 505 510

Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe Thr Ser  
 515 520 525  
 Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu Glu Trp  
 530 535 540  
 Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp Thr Leu  
 545 550 555 560  
 Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg Glu Leu  
 565 570 575  
 Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu Ser Lys  
 580 585 590  
 Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser Asp Ile  
 595 600 605  
 Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser Arg Gln  
 610 615 620  
 Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly Pro Ser Ala  
 625 630 635 640  
 Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile Asp Leu  
 645 650 655  
 Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met Ala Arg  
 660 665 670  
 Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro Gly Gly  
 675 680 685  
 Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg Ser Ser  
 690 695 700  
 Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu Gln Lys  
 705 710 715 720  
 Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln Gly Asp  
 725 730 735  
 Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu Ala Ala  
 740 745 750  
 Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala Ala Leu  
 755 760 765  
 Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser Gly Ser  
 770 775 780  
 Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val Thr Thr  
 785 790 795 800  
 Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe Gln Asn  
 805 810 815

Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly His  
 820 825 830  
 Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His His  
 835 840 845  
 His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr Phe Ala  
 850 855 860  
 Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val Pro  
 865 870 875 880  
 Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp Glu  
 885 890 895  
 Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu Gln  
 900 905 910  
 Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly Pro  
 915 920 925  
 Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly Gly Gly Ser  
 930 935 940  
 Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys Ser  
 945 950 955 960  
 Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser Gly  
 965 970 975  
 Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro Arg  
 980 985 990  
 Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly Ser  
 995 1000 1005  
 Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln His  
 1010 1015 1020  
 Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu Arg  
 1025 1030 1035 1040  
 Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile Glu  
 1045 1050 1055  
 Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser Lys  
 1060 1065 1070  
 Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu Glu  
 1075 1080 1085  
 Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu Glu  
 1090 1095 1100  
 Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys Ile  
 1105 1110 1115 1120

Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg Leu Arg  
 1125 1130 1135  
 Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile Gly Arg  
 1140 1145 1150  
 Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro Ala Met Ala  
 1155 1160 1165  
 Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg Gly  
 1170 1175 1180  
 Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro His Leu  
 1185 1190 1195 1200  
 Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly Cys Arg  
 1205 1210 1215  
 Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser Pro Pro  
 1220 1225 1230  
 Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro Pro Ser  
 1235 1240 1245  
 Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser Pro Thr  
 1250 1255 1260  
 Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro Leu Thr  
 1265 1270 1275 1280  
 Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser Arg Arg  
 1285 1290 1295  
 Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His Leu Pro  
 1300 1305 1310  
 His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro  
 1315 1320 1325

<210> 7  
 <211> 216  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: mammalian  
 SYNGAP-C

<400> 7  
 Gly Lys Ala Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp  
 1 5 10 15  
 Arg Phe Met Glu Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala  
 20 25 30

Thr Lys Ala Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu  
 35 40 45  
 Lys Asp Ala Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu  
 50 55 60  
 Asn Cys Glu Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu  
 65 70 75 80  
 His Gln Ala Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val  
 85 90 95  
 Val Asn Ser His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala  
 100 105 110  
 Ser Trp Arg Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp  
 115 120 125  
 Arg Leu Ile Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile  
 130 135 140  
 Met Ser Pro Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln  
 145 150 155 160  
 Thr Ser Arg Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala  
 165 170 175  
 Asn Phe Ser Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn  
 180 185 190  
 Glu Phe Leu Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu  
 195 200 205  
 Ile Ser Asn Leu Asp Thr Leu Thr  
 210 215

<210> 8  
 <211> 218  
 <212> PRT  
 <213> Rattus norvegicus

<400> 8  
 Lys Leu Glu Ser Leu Leu Leu Cys Thr Leu Asn Asp Arg Glu Ile Ser  
 1 5 10 15  
 Met Glu Asp Glu Ala Thr Thr Leu Phe Arg Ala Thr Thr Leu Ala Ser  
 20 25 30  
 Thr Leu Met Glu Gln Tyr Met Lys Ala Thr Ala Thr Gln Phe Val His  
 35 40 45  
 His Ala Leu Lys Asp Ser Ile Leu Lys Ile Met Glu Val Gln His Lys  
 50 55 60  
 Trp Pro Thr Asn Asn Thr Met Arg Thr Arg Val Val Ser Gly Phe Val  
 65 70 75 80

```
<210> 9
<211> 219
<212> PRT
<213> Homo sapiens
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```

<400> 9
His Leu Leu Tyr Gln Leu Leu Trp Asn Met Phe Ser Lys Glu Val Glu
  1             5             10             15

Leu Ala Asp Ser Met Gln Thr Leu Phe Arg Gly Asn Ser Leu Ala Ser
          20             25             30

Lys Ile Met Thr Phe Cys Phe Lys Val Tyr Gly Ala Thr Tyr Leu Gln
          35             40             45

Lys Leu Leu Asp Pro Leu Leu Arg Ile Val Ile Thr Ser Ser Asp Trp
  50             55             60

Gln His Val Ser Phe Glu Val Asp Pro Thr Arg Leu Glu Pro Ser Glu
  65             70             75             80

Ser Leu Glu Glu Asn Gln Arg Asn Leu Leu Gln Met Thr Glu Lys Phe
          85             90             95

Phe His Ala Ile Ile Ser Ser Ser Ser Glu Phe Pro Pro Gln Leu Arg
          100            105            110

Ser Val Cys His Cys Leu Tyr Gln Val Val Ser Gln Arg Phe Pro Gln
          115            120            125

```



Asn Ser Ile Gly Ala Val Gly Ser Ala Met Phe Leu Arg Phe Ile Asn  
 130 135 140

Pro Ala Ile Val Ser Pro Tyr Glu Ala Gly Ile Leu Asp Lys Lys Pro  
 145 150 155 160

Pro Pro Arg Ile Glu Arg Gly Leu Lys Leu Met Ser Lys Ile Leu Gln  
 165 170 175

Ser Ile Ala Asn His Val Leu Phe Thr Lys Glu Glu His Met Arg Pro  
 180 185 190

Phe Asn Asp Phe Val Lys Ser Asn Phe Asp Ala Ala Arg Arg Phe Phe  
 195 200 205

Leu Asp Ile Ala Ser Asp Cys Pro Thr Ser Asp  
 210 215

<210> 10  
 <211> 82  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: mammalian  
 SYNGAP-A

<400> 10  
 Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala  
 1 5 10 15

Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Lys Lys Pro  
 20 25 30

Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr  
 35 40 45

Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp  
 50 55 60

Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn  
 65 70 75 80

Ser Arg

<210> 11  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Phe Tyr Lys Asn Ile Val Lys Lys Gly Tyr Leu Leu Lys Lys Gly Lys  
 1 5 10 15

Gly Lys Arg Trp Lys Asn Leu Tyr Phe Ile Leu Glu Gly Ser Asp Ala  
 20 25 30

Pro Gly

<400> 12

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<210> 13
<211> 108
<212> PRT
<213> Homo sapiens
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<400> 13

Met Glu Pro Lys Arg Ile Arg Glu Gly Tyr Leu Val Lys Lys Gly Ser  
1 5 10 15

Val Phe Asn Thr Trp Lys Pro Met Trp Val Val Leu Leu Glu Asp Gly  
                   20                  25                  30  
 Ile Glu Phe Tyr Lys Lys Lys Ser Asp Asn Ser Pro Lys Gly Met Ile  
                   35                  40                  45  
 Pro Leu Lys Gly Ser Thr Leu Thr Ser Pro Cys Gln Asp Phe Gly Lys  
                   50                  55                  60  
 Arg Met Phe Val Phe Lys Ile Thr Thr Thr Lys Gln Gln Asp His Phe  
                   65                  70                  75                  80  
 Phe Gln Ala Ala Phe Leu Glu Glu Arg Asp Ala Trp Val Arg Asp Ile  
                   85                  90                  95  
 Asn Lys Ala Ile Lys Cys Ile Glu Gly Gly Gln Lys  
                   100                  105

<210> 14  
 <211> 110  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: mammalian  
 SYNGAP-A

<400> 14  
 Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu Leu Pro  
   1                  5                  10                  15  
 Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met Leu Tyr  
                   20                  25                  30  
 Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr Val Phe  
                   35                  40                  45  
 Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg Ala Leu  
                   50                  55                  60  
 Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys Asp Lys  
                   65                  70                  75                  80  
 Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu Ala Gly  
                   85                  90                  95  
 Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr  
                   100                  105                  110

<210> 15  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 15

Gln Val Ser Ser Leu Val Leu His Ile Glu Glu Ala His Lys Leu Pro  
 1 5 10 15

Val Lys His Phe Thr Asn Pro Tyr Cys Asn Ile Tyr Leu Asn Ser Val  
 20 25 30

Gln Val Ala Lys Thr His Ala Arg Glu Gly Gln Asn Pro Val Trp Ser  
 35 40 45

Glu Glu Phe Val Phe Asp Asp Leu Pro Pro Asp Ile Asn Arg Phe Glu  
 50 55 60

Ile Thr Leu Ser Asn Lys Thr Lys Lys Ser Lys Asp Pro Asp Ile Leu  
 65 70 75 80

Phe Met Arg Cys Gln Leu Ser Arg Leu Gln Lys Gly His Ala Thr Asp  
 85 90 95

Glu Trp Phe Leu Leu Ser Ser His Ile Pro Leu  
 100 105

&lt;210&gt; 16

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 16

Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val Leu Gln Ala  
 1 5 10 15

Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr Val  
 20 25 30

Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Tyr Glu Thr Lys Val  
 35 40 45

His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe Thr Phe Lys  
 50 55 60

Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met Ala Ile Tyr  
 65 70 75 80

Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Val Lys Val  
 85 90 95

Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu Trp Arg Asp  
 100 105 110

Leu Gln Gly Gly  
 115

&lt;210&gt; 17

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Bos taurus

&lt;400&gt; 17

Leu Tyr Asp Gln Asp Asn Ser Ser Leu Lys Cys Thr Ile Ile Lys Ala  
 1 5 10 15

Lys Gly Leu Lys Pro Met Asp Ser Asn Gly Leu Ala Asp Pro Tyr Val  
 20 25 30

Lys Leu His Leu Leu Pro Gly Ala Ser Lys Ser Asn Lys Leu Arg Thr  
 35 40 45

Lys Thr Leu Arg Asn Thr Arg Asn Pro Ile Trp Asn Glu Thr Leu Val  
 50 55 60

Tyr His Gly Ile Thr Asp Glu Asp Met Gln Arg Lys Thr Leu Arg Ile  
 65 70 75 80

Ser Val Cys Asp Glu Asp Lys Phe Gly His Asn Glu Phe Ile Gly Glu  
 85 90 95

Thr Arg Phe Ser Leu Lys Lys Leu Lys Pro Asn Gln Arg Lys Asn Phe  
 100 105 110

Asn Ile Cys Leu Glu Arg Val Ile Pro Met Lys Arg Ala Gly Thr Thr  
 115 120 125

Gly Ser Ala Arg  
 130

&lt;210&gt; 18

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:  
 Oligonucleotide

&lt;400&gt; 18

acgcgtcgac cagagagccc cgcaag

26

&lt;210&gt; 19

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:  
 Oligonucleotide

&lt;400&gt; 19

gaagatctag gtctatactg ggccac

26

&lt;210&gt; 20

&lt;211&gt; 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 20

Lys Arg Leu Leu Asp Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln  
1 5 10 15

Gln Thr Arg Val  
20

<210> 21

<211> 1135

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian  
SYNGAP-C

<400> 21

Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro  
1 5 10 15

Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile  
20 25 30

Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu  
35 40 45

Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala  
50 55 60

Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn  
65 70 75 80

Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile  
85 90 95

Glu Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys  
100 105 110

Leu Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala  
115 120 125

Ser Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu  
130 135 140

Pro Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys  
145 150 155 160

Lys Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro  
165 170 175

Val Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val  
 180 185 190  
 Thr Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly  
 195 200 205  
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys  
 210 215 220  
 Pro Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro  
 225 230 235 240  
 Met Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg  
 245 250 255  
 Met Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu  
 260 265 270  
 Glu Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala  
 275 280 285  
 Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met  
 290 295 300  
 Glu Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala  
 305 310 315 320  
 Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala  
 325 330 335  
 Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu  
 340 345 350  
 Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala  
 355 360 365  
 Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser  
 370 375 380  
 His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg  
 385 390 395 400  
 Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile  
 405 410 415  
 Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro  
 420 425 430  
 Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg  
 435 440 445  
 Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser  
 450 455 460  
 Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu  
 465 470 475 480



Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn  
 485 490 495  
 Leu Asp Thr Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu  
 500 505 510  
 Gly Arg Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro  
 515 520 525  
 Gln Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu  
 530 535 540  
 Leu Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln  
 545 550 555 560  
 Pro Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg  
 565 570 575  
 Gly Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser  
 580 585 590  
 Ser Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met  
 595 600 605  
 Asp Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro  
 610 615 620  
 Pro Pro Gly Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu  
 625 630 635 640  
 Ala Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu  
 645 650 655  
 Pro Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp  
 660 665 670  
 Leu Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser  
 675 680 685  
 Asn Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu  
 690 695 700  
 Thr Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln  
 705 710 715 720  
 Gly Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met  
 725 730 735  
 Gly Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu  
 740 745 750  
 Ser Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro  
 755 760 765  
 Pro Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His  
 770 775 780

His 785	His	His	His	His	His 790	His	His	His	His	Arg	Gly 795	Gly	Glu	Pro	Pro	Gly 800
Asp	Thr	Phe	Ala	Pro 805	Phe	His	Gly	Tyr	Ser 810	Lys	Ser	Glu	Asp	Leu	Ser 815	
Thr	Gly	Val	Pro 820	Lys	Pro	Pro	Ala	Ala 825	Ser	Ile	Leu	His	Ser 830	His	Ser	
Tyr	Ser	Asp 835	Glu	Phe	Gly	Pro	Ser 840	Gly	Thr	Asp	Phe	Thr 845	Arg	Arg	Gln	
Leu 850	Ser	Leu	Gln	Asp	Asn	Leu	Gln 855	His	Met	Leu	Ser 860	Pro	Pro	Gln	Ile	
Thr 865	Ile	Gly	Pro	Gln	Arg 870	Pro	Ala	Pro	Ser	Gly 875	Pro	Gly	Gly	Gly	Ser 880	
Gly	Gly	Gly	Ser	Gly 885	Gly	Gly	Gly	Gly	Gly	Gln 890	Pro	Pro	Pro	Leu	Gln 895	
Arg	Gly	Lys	Ser 900	Gln	Gln	Leu	Thr	Val 905	Ser	Ala	Ala	Gln	Lys 910	Pro	Arg	
Pro	Ser	Ser 915	Gly	Asn	Leu	Leu	Gln 920	Ser	Pro	Glu	Pro	Ser 925	Tyr	Gly	Pro	
Ala 930	Arg	Pro	Arg	Gln	Gln	Ser 935	Leu	Ser	Lys	Glu	Gly 940	Ser	Ile	Gly	Gly	
Ser 945	Gly	Gly	Ser	Gly	Gly 950	Gly	Gly	Gly	Gly	Gly 955	Leu	Lys	Pro	Ser	Ile 960	
Thr	Lys	Gln	His	Ser 965	Gln	Thr	Pro	Ser	Thr 970	Leu	Asn	Pro	Thr	Met 975	Pro	
Ala	Ser	Glu	Arg 980	Thr	Val	Ala	Trp	Val 985	Ser	Asn	Met	Pro	His 990	Leu	Ser	
Ala	Asp	Ile	Glu	Ser	Ala	His	Ile 1000	Glu	Arg	Glu	Glu 1005	Tyr	Lys	Leu	Lys	
Glu 1010	Tyr	Ser	Lys	Ser	Met	Asp 1015	Glu	Ser	Arg	Leu	Asp 1020	Arg	Val	Lys	Glu	
Tyr 1025	Glu	Glu	Glu	Ile	His	Ser	Leu	Lys	Glu 1035	Arg	Leu	His	Met	Ser	Asn 1040	
Arg	Lys	Leu	Glu	Glu	Tyr	Glu	Arg	Arg 1050	Leu	Leu	Ser	Gln	Glu	Glu	Gln 1055	
Thr	Ser	Lys 1060	Ile	Leu	Met	Gln	Tyr	Gln 1065	Ala	Arg	Leu	Glu	Gln 1070	Ser	Glu	
Lys 1075	Arg	Leu	Arg	Gln	Gln	Gln	Val 1080	Glu	Lys	Asp	Ser	Gln	Ile	Lys	Ser 1085	

Ile Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His  
1090 1095 1100

Pro Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp  
1105 1110 1115 1120

Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val  
1125 1130 1135

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